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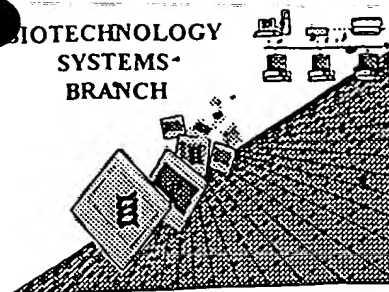
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RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS-
BRANCH



0590
10/7

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/963314
Source: OIPE
Date Processed by STIC: 10/10/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/963314

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid ~~<213>~~ ~~<223>~~
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). ~~<220>-<223> section is required when <213> response is Unknown or Artificial Sequence~~
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 10/10/2001

PATENT APPLICATION: US/09/963,314

TIME: 14:09:28

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10102001\I963314.raw

4 <110> APPLICANT: Lee, Sang Yup
 5 Choi, Jong Gil
 7 <120> TITLE OF INVENTION: DNA CHIP USING CODON SCANNING ALGORITHM
 10 <130> FILE REFERENCE: HYLEE55.001AUS
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/963,314 *ok*
 C--> 12 <141> CURRENT FILING DATE: 2001-09-25
 12 <150> PRIOR APPLICATION NUMBER: KOREA 10-2000-57208
 13 <151> PRIOR FILING DATE: 2000-09-29
 15 <160> NUMBER OF SEQ ID NOS: 14
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 19
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Artificial Sequence ✓
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: primer 1 ✓
 27 <400> SEQUENCE: 1
 28 gccctgtgac attcttcga
 30 <210> SEQ ID NO: 2
 31 <211> LENGTH: 19
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Artificial Sequence ✓
 35 <220> FEATURE:
 36 <223> OTHER INFORMATION: primer 2 ✓
 38 <400> SEQUENCE: 2
 39 gctgctgtta cctttgccca
 41 <210> SEQ ID NO: 3
 42 <211> LENGTH: 20
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Artificial Sequence ✓
 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: primer 3 ✓
 49 <400> SEQUENCE: 3
 50 gatgtttgac aagactggca
 52 <210> SEQ ID NO: 4
 53 <211> LENGTH: 21
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial Sequence ✓
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: primer 4 ✓
 60 <400> SEQUENCE: 4
 61 cctctttaca gtatttggtg a
 63 <210> SEQ ID NO: 5
 64 <211> LENGTH: 19
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Artificial Sequence ✓
 68 <220> FEATURE:

Does Not Comply
Corrected Diskette Needed

See Error Summary Sheet
See Explanations pages 2 and 3

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/963,314

DATE: 10/10/2001

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10102001\I963314.raw

69 <223> OTHER INFORMATION: primer 5 ✓
 71 <400> SEQUENCE: 5
 72 caatcgacaga cgctgtcaa 19
 74 <210> SEQ ID NO: 6
 75 <211> LENGTH: 19
 76 <212> TYPE: DNA
 77 <213> ORGANISM: Artificial Sequence ✓
 79 <220> FEATURE:
 80 <223> OTHER INFORMATION: primer 6 ✓
 82 <400> SEQUENCE: 6
 83 ctgtacctgg gtggcaata 19
 85 <210> SEQ ID NO: 7
 86 <211> LENGTH: 20
 87 <212> TYPE: DNA
 88 <213> ORGANISM: Artificial Sequence ✓
 90 <220> FEATURE:
 91 <223> OTHER INFORMATION: primer 7 ✓
 93 <400> SEQUENCE: 7
 94 taaaggggaag aaagtcgcca 20
 96 <210> SEQ ID NO: 8
 97 <211> LENGTH: 18
 98 <212> TYPE: DNA
 99 <213> ORGANISM: Artificial Sequence ✓
 101 <220> FEATURE:
 102 <223> OTHER INFORMATION: primer 8 ✓
 104 <400> SEQUENCE: 8
 105 gctgcctcga tggccaca 18
 107 <210> SEQ ID NO: 9
 108 <211> LENGTH: 16
 109 <212> TYPE: DNA
 110 <213> ORGANISM: Artificial Sequence ✓
 112 <220> FEATURE:
 113 <223> OTHER INFORMATION: tgcctggaag tccgtgca
 114 18
 116 <400> SEQUENCE: 9
 117 cagccaccgg cccagg
 119 <210> SEQ ID NO: 10
 120 <211> LENGTH: 17
 121 <212> TYPE: DNA
 122 <213> ORGANISM: Artificial Sequence
 124 <220> FEATURE:
 125 <223> OTHER INFORMATION: Ctttcacttc acccctct
 126 18
 128 <400> SEQUENCE: 10
 129 ccagccacag gccagg
 131 <210> SEQ ID NO: 11
 132 <211> LENGTH: 19
 133 <212> TYPE: DNA
 134 <213> ORGANISM: Artificial Sequence

1. Invalid 223 response
Nucleotide bases must appear
below field 400
2. Artificial Sequence must be
explained in field 223
3. Integer in field 211 must match
number of bases in sequence
1. Invalid 223 response
Nucleotide bases must appear
below field 400
2. Artificial Sequence must be
explained in field 223
3. Integer in field 211 must match
number of bases in sequence

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/963,314

DATE: 10/10/2001

TIME: 14:09:28

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10102001\I963314.raw

136 <220> FEATURE:
 137 <223> OTHER INFORMATION: gagcacagag ccatgtgca
 138 19
 140 <400> SEQUENCE: 11
 141 ctacgtctag gagaagcca
 143 <210> SEQ ID NO: 12
 144 <211> LENGTH: 19
 145 <212> TYPE: DNA
 146 <213> ORGANISM: Artificial Sequence ✓
 148 <220> FEATURE:
 149 <223> OTHER INFORMATION: primer 10 ✓
 151 <400> SEQUENCE: 12
 152 gagcacagag ccatgtgca
 154 <210> SEQ ID NO: 13
 155 <211> LENGTH: 18
 156 <212> TYPE: DNA
 157 <213> ORGANISM: Artificial Sequence ✓
 159 <220> FEATURE:
 160 <223> OTHER INFORMATION: primer 11 ✓
 162 <400> SEQUENCE: 13
 163 ctttcacttc acccctct
 165 <210> SEQ ID NO: 14
 166 <211> LENGTH: 18
 167 <212> TYPE: DNA
 168 <213> ORGANISM: Artificial Sequence ✓
 170 <220> FEATURE:
 171 <223> OTHER INFORMATION: primer 12 ✓
 173 <400> SEQUENCE: 14
 174 tgcctggaag tccgtgca

1. Invalid 223 response
Nucleotide bases must appear
beneath field 400
2. Artificial Sequence must be
explained on field 223
3. Integer in field 211 must
match number of nucleotide
bases in sequence.

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/963,314

DATE: 10/10/2001

TIME: 14:09:29

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\10102001\I963314.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date